

Shubler

BIOTECHNOLOGY
SYSTEMS
BRANCH



#13
Linda
8/18/00

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/101,423

Source: 1632

Date Processed by STIC: 8/9/2000

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR FURTHER INFORMATION, PLEASE TELEPHONE MARK SPENCER, 703-308-4212.

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
<http://www.uspto.gov/web/offices/pac/checker>

Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/101,423

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 Wrapped Aminos The amino acid number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes space.
- 4 Misaligned Amino Acid Numbering The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 Variable Length Sequence(s) contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
- 7 PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 8 Skipped Sequences (OLD RULES) Sequence(s) missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 Skipped Sequences (NEW RULES) Sequence(s) missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 10 Use of n's or Xaa's (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 Use of <213>Organism (NEW RULES) Sequence(s) 2 are missing this mandatory field or its response.
- 12 Use of <220>Feature (NEW RULES) Sequence(s) are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

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R. Shukla

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1632

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/101,423

TECH CENTER 1600/2900
DATE: 08/09/2000
TIME: 14:53:45

error throughout.

Input Set : A:\ES.txt
Output Set: N:\CRF3\08092000\I101423.raw

Does Not Comply
Corrected Diskette Needed

3 <110> APPLICANT: Rudland, Philip S.
4 Barracclough, Roger B.
W--> 5 <120> TITLE OF INVENTION: Metastasis Inducing DNA=s
W--> 6 <130> FILE REFERENCE: WPT 0114 PUS
W--> 7 <140> CURRENT APPLICATION NUMBER: US 09/101,423
8 <141> CURRENT FILING DATE: 1998-11-27
9 <150> PRIOR APPLICATION NUMBER: PCT/GB97/00074
10 <151> PRIOR FILING DATE: 1997-01-10
W--> 11 <160> NUMBER OF SEQ ID: 6

*See Item 5
on Error Summary
sheet*

ERRORED SEQUENCES

13 <210> SEQ ID NO: 1
14 <211> LENGTH: 1033 base pairs
15 <212> TYPE: DNA
16 <213> ORGANISM: Homo sapiens
18 <400> SEQUENCE: 1
E--> 19 cttccttggg gctctatgtc ttgcctctcc cttctccag tcccattaag
20 ccataaccat 60
E--> 22 cttgacagac tctgggacag tcccctctgc tctcctgttg ggcctgagt
23 ccccttttgc 120
E--> 25 ctgaggaccc ttcacgtage ctcccatctg gatgacctag tagaagacgt
26 gggaagtgt 180
E--> 28 cacactcagg taactgagca gagctcagag atttaaagtg agtctgggga
29 gcctcgagga 240
E--> 32 ttgatctgct gccttaaaaa gccaatgga tgaactaacc agactattgt
33 cacttttaggt 300
E--> 35 gggaagtcac tagcatatct gatgggtcac atctgagaaa ggtttctagc
36 agtgggtggc 360
E--> 38 ttgtgtgagc agcatggcgt gtatcatggt gtgcagcata ctcaggctgc
39 ttgcaacact 420
E--> 41 cgaggetctt cttcagtatt aggggaacca ctggtgttga acatggtcca
42 agaatacagt 480
E--> 44 catgtgagga gaatcccaat gcgtcaggag aaaacgagag tctgtgacct
45 ccattcttca 540
E--> 47 agatacagaa ttattcttgg actgtgtttt catgctcctt gtggatggga
48 gtgagtttac 600
E--> 50 ttcagggttaa tcagcattgc ttactgttgg tattcaagta aatgcttaaa
51 ttatcctgga 660
E--> 53 tatacctctg tgggaagcag gtttttgata catgcagctt gtccttgtga
54 ttgatactgc 720
E--> 56 ttgaactcaa gagaactttg ctcatgtgat ctttcttaac cgatggagta
57 gaaactgtct 780
E--> 59 gatgctctca ataaagtgg ctcttgcaag agacgttagt ctgtcctgtt
60 tatctgtctc 840
E--> 63 attcttccgc tcccacggcc tctacagcac taaaccacc accgatagac

*format
error*

*see Item 1 on Error
summary sheet*

*Please ensure
all bases are in
lower-case letters,
per new sequence
Run format.*

*The CRF program
converted letters to
lower-case.*

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/101,423

DATE: 08/09/2000
TIME: 14:53:45

Input Set : A:\ES.txt
Output Set: N:\CRF3\08092000\I101423.raw

64 tcagtctttc 900
E--> 66 actgacaaac atcaccagag gctcttaact gagattataa actgttacta
67 gatgatgggt 960
E--> 69 ggaatcgctc cccagaaaca taaacattta cttggagaac tcaagacccc
70 tttgtagaca 1020
72 taactcccat ggt
74 <210> SEQ ID NO: 2
75 <211> LENGTH: 1058 base pairs
76 <212> TYPE: DNA
W--> 78 <213> ORGANISM: *mandatory name identifier and response*
78 <400> SEQUENCE: 2
E--> 79 attgctgtga gcctattagc gacatttggg gacgcccctt ttaagggggg
80 agatacaaag 60
E--> 82 aatgggttga aattctgtgc cacaacgct ctccatgttt tcacaattac
83 acttgcaacc 120
E--> 85 tgtggtcagc agccagaatt tagggatgtg atgggacagg gtcggggaaa
86 gaaggagaag 180
E--> 88 ggtaaaggaa agacagcacg ttaaagtcca aacagctcca ggagactatc
89 tgtagaataa 240
E--> 91 acatcagacc atgaggagaa ttgatcatcat tgtttttcaa tgggtatcgc
92 caagggaact 300
E--> 95 ttccatctga ttaaaaataa ttactgctgg cactaaatcc aattggaaat
96 gcccacaca 360
E--> 98 atttatcttc cacttcatgc tgctaccata tgctgacgt ggcggagcag
99 aagcattccc 420
E--> 101 tcccgttctg ataaatagta ctttgtaaatt atttgagac gggagctctg
102 gtgacagga 480
E--> 104 acacgtacaa accggcctgt ttatcatgtt cccgatagag gccctctttg
105 acgtacagga 540
E--> 107 ccccaaaaca gtcaggatgc tgtgaatttc ctccatgaa gccttgttca
108 caattagcaa 600
E--> 110 ccattggagg aagcaggctg cactgtctac cacaagtggc actttccaaa
111 gagcacacat 660
E--> 113 atattggagc aagacatttt gctggctgac tgggtgctgtg taagctgata
114 aactgctata 720
E--> 116 tttattaaac tggcttttct ttgaacaccc cactcaagga aaaaaaaca
117 cacttagggg 780
E--> 119 gacattattt ggagatgaag tctttataga gatgcttaag tttaaacgag
120 acttttaaag 840
E--> 122 cggctctat tccatttaat gaatggtgct cctacaaagg aagaaactgg
123 gacagaggta 900
E--> 126 tgtacacttg tgtgtgtgtg agagacaacg tgaggagctg aagaggagca
127 cgtacaagtc 960
E--> 129 agagaaaggc tgacccttat tcacactgag caaaccagtc atgtgtgggt
130 cgatagatga 1020
132 gagtatcccc caagactcac acattcgaac gcttggtc
134 <210> SEQ ID NO: 3
135 <211> LENGTH: 1008 base pairs
136 <212> TYPE: DNA

1033

same error
(see items 11 and 12 on Error Summary Sheet)

same format error

1058

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/101,423

DATE: 08/09/2000
TIME: 14:53:45

Input Set : A:\ES.txt
Output Set: N:\CRF3\08092000\I101423.raw

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137 <213> ORGANISM: Homo sapiens
139 <400> SEQUENCE: 3
E--> 140 aggaccagag ttcacatccc atcaaatggc ccagaagggtt ttaatgctgt
141 cttttggccc 60
E--> 143 agggcggaac tgcacacaca tgtgcacata cacttacaga gacacacatt
144 cagcagcata 120
E--> 146 agaacacaat cacaaataaa aaaaatcttg aaaaatttta agctaaaatt
147 gttaagaaat 180
E--> 149 aacatatata caatttttct ttattttttt aaagatttat ttattttaatg
150 tatatgagta 240
E--> 152 cactgcctct ccctccagac atagcagtag agggcatcgg atcccattac
153 agatgggtgt 300
E--> 155 gagccaccat gtgggtttcac agatgggtgt gagccaccat gtgggtttcag
156 gaattgaact 360
E--> 158 caggaccctt ggaagagcag tcagtgtctt taacctctaa gccatctctc
159 ctgaccctta 420
E--> 161 tatacaattt taatgctacg tacacacaac ttctctttcc tttaatgggt
162 gagatttttg 480
E--> 164 tctggagaag taagaataaa ggagggaag aacattgctt tcacattgca
165 ccagtgggaa 540
E--> 167 cagcgtgttt aaagttagaa tgccatgaaa tgactggcct gccttctcat
168 tactgttctt 600
E--> 170 cccactcttc cttttaactg gagctccttt atctaattta ttagtttgac
171 gatacccagg 660
E--> 173 gttttcttct gttttgatct ttttaagaca gagactcacc atatagccct
174 ggcgtggcctg 720
E--> 176 aagctcacta ttagaccagc tctggccttg aactcaaagg agatctatct
177 gcttcctagt 780
E--> 179 gctgggatta aaggcttggt ctaccaagtc tggctctgagg ctttggagca
180 gcctcggttt 840
E--> 182 tggecttctt taaggatctc taagctagca gtaagtagcc tagccatgct
183 gttgtaggaa 900
E--> 185 gttgttcgtt catcctggct ccagcacaaa ggcagtcact aaacgtcggc
186 ctcatttcat 960
E--> 189 cagagctgaa tgcaaattcc ttgtgtctct cctgtgtcct cctggaac
E--> 190 1008
192 <210> SEQ ID NO: 4
193 <211> LENGTH: 1088 base pairs
194 <212> TYPE: DNA
195 <213> ORGANISM: Homo sapiens
197 <400> SEQUENCE: 4
E--> 198 agttggggac acagcttgct tgattaagat gtttcttggg aaaaggagtt
199 aagcctaattg 60
E--> 201 atttccaatg gaaaggactg ctaattgggg aggcaatggt gcttaattgg
202 gacacctgcg 120
E--> 204 ggtaattaaa agctctctcc cagtggcctt tctgttttt ggctctggga
205 ggcgaaggca 180
E--> 207 ttgagaggga tgcaggcatt ctaagggtcg gttcttgggt tctcccttcc
208 cctctgtcca 240

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/101,423

DATE: 08/09/2000
TIME: 14:53:45

Input Set : A:\ES.txt
Output Set: N:\CRF3\08092000\I101423.raw

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E--> 210 aactcagtga ggtatccctg tctgtgctgt ccttagagt cgtcctgag
211 gccttggtga 300
E--> 213 gttaaggctc ctggatctga gctgcctcag ggaaacgcat gagtcattg
214 gaaaggggag 360
E--> 216 aaccaggcaa aggtgttggc tgtgacctca gaattctgag gggcaaaggt
217 tcaaggctaa 420
E--> 220 ctctcattat agagcaagtt tgagactggc ctgggaacaa aaatataaag
221 tgagtgaagt 480
E--> 223 catatgacag cacctgagga gtccctgtccc tagagatcat aaggacctgg
224 ctgctgggga 540
E--> 226 cttgttgag atggcacttt gtgtcgagag aggggacctg ccccgacatg
227 ggaggccctg 600
E--> 229 gaagatcctc tggattaact gtgaacactg attgctgctt tatacctgga
230 gttgtgctgt 660
E--> 232 tatctggtac acatctgctg ggtgaatgag ttcatgggct ttatttcagt
233 gaggtattta 720
E--> 235 cctgaggaga aagaaggact ggtgccacaa agcacagctt ttaaactctgt
236 gggttgtgac 780
E--> 238 ccattatgga ctatcataac tgagtgcagg tatcaagaat acttttagcag
239 gtggtaaaaa 840
E--> 241 gatttttgaa tgcgcaacga ccaaaactga actcaaaaat caagcatggc
242 atggatcctg 900
E--> 244 ggtgctcctg gaagcacttg cctttactgc attgtgcgac ttgacggtag
245 ccttggttct 960
E--> 247 gaatgcacaa cacgtgggct ttgggctgca caggccacca cgcctgacct
248 gaaacacctc 1020
E--> 251 agctcagggt tgtggctatg tctatgact tggacttact tttattgcac
252 atataaatat 1080
254 tttcctgc 1088
257 <210> SEQ ID NO: 5
258 <211> LENGTH: 960 base pairs
259 <212> TYPE: DNA
260 <213> ORGANISM: Homo sapiens
262 <400> SEQUENCE: 5
E--> 263 gagggggtgg tggcacagtt atgtttttgt aggaaggggt ccatgaacct
264 cagcagagct 60
E--> 266 cgggttagaa atttaaaagc cctgagggga attttttttt taaatcgcta
267 tgaatctgac 120
E--> 269 atgagaaaaa cagatcagaa acgttcttgt gcttcagaaa aggacaagtg
270 tgtgagctaa 180
E--> 272 cagactgcac actggtgttc gaggcacatc tggatcacag gagcgtcaga
273 taatgtcccc 240
E--> 275 aaaggtaaat gcatttgctt gcacagtacc gagtgtgggt ggggggtgct
276 acagcccagc 300
E--> 278 ggttctcaac ctctctgatg ctctgacct ttaatacagt gcctcatgct
279 ctggtgacct 360
E--> 281 ccccaacctt aaaattattt ttgttgctgt tcataactgt gattttgata
282 ctgttatgaa 420
E--> 284 ttgtaataa aataattttg aagaaagagg ttgccaagg gtttgagaac

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/101,423

DATE: 08/09/2000
TIME: 14:53:45

Input Set : A:\ES.txt
Output Set: N:\CRF3\08092000\I101423.raw

285 tgctgttcta 480
E--> 287 gccccacgtg gatggttttt cgtcatttgg ggtttttatg aggcagagtc
288 ttatgtagcc 540
E--> 290 caggctagca gcctagaatg tgctacttag ctgaggaata accttggaac
291 ttctgaggac 600
E--> 293 tggagagact ggcttagtcc tcaagaaact ggaaatagct ggagtttggc
294 tacttgtggg 660
E--> 296 ttcccttttc ttcaaacctt ttctactctt ttccaccct gtcggccccc
297 taacactaaa 720
E--> 299 taagaaagag aaaggggagc atagagggga aaagaaaccc ctgaataacg
300 tcagtagttg 780
E--> 302 gcaaaggggg gtgacatatg ttgtcattag accacatcct ggtgattaag
303 gggagtcaag 840
E--> 305 ttccctgggg caagtttgat ctttcgtgta acgatatcta atttcttctc
306 cctgttgctt 900
E--> 308 cgtctttgtg aacaacgact tgataacca caatggacca tcaaccaacc
309 aaccaaccat 960
311 <210> SEQ ID NO: 6
312 <211> LENGTH: 1090 base pairs
313 <212> TYPE: DNA
314 <213> ORGANISM: Homo sapiens
316 <400> SEQUENCE: 6
E--> 317 ttgtctctgg tgttacttgt ttcccatctt ctgacagtgg tttagacctc
318 tatagcctg 60
E--> 320 tgtgtcagga gtgtgtaga cctattttcc tgttttcttt cagccagtta
321 caggaacaga 120
E--> 323 gtgttctact gtcagatgtg tagctgttcc tgtccactga ctttcaagct
324 gtctctgtgt 180
E--> 326 gcaggaacca gaagggcctg tccctacttc tactgggccc ctacgcacag
327 ggggcctaga 240
E--> 329 tgggtgctagg tgttttcttc tagagcctga aatgtgggca gagagtagtc
330 tctctgtggt 300
E--> 332 tcttaggtat gtcttccctc ctgaaggctt agctctccct tccatgggat
333 atgggtgcag 360
E--> 335 ggagctgttt gaccaggtcc tctcaaatcc ggggtgcagtc tggaccgcag
336 gctcctgtag 420
E--> 338 cttgcctgct gcaatcttcc cgcacccaga ggcacccaag ttctctcttg
339 ggccaaggat 480
E--> 341 gtgggcaaaag gtgggcagaa gtggcaatct ctctgcctc agcgtctcag
342 gattgcctc 540
E--> 344 acttctgggc aatccgctct ctctccaca gggtttggga gcagggagct
345 gtgggccggt 600
E--> 348 atcaggcaaa ggtttgaggc aaccagttag aaactggaag tgtcaggtcc
349 cagaggaatt 660
E--> 351 ttgcctttgt gtgtcctgag tccaccaggc aggtcacttg gagcagaaaa
352 attggtttct 720
E--> 354 cctcgggtct caggcctgaa gttgcacctc agggttggct ttcagctgta
355 cctgtggaaa 780
E--> 357 gtatggtttt aaaaatctaa gatagctatc atgcagcaag gcttgtgtaa

same

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same

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/101,423

DATE: 08/09/2000
 TIME: 14:53:45

Input Set : A:\ES.txt
 Output Set: N:\CRF3\08092000\I101423.raw

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358 aatgtctatt 840
 E--> 360 tggttccttt atgacttact ttgtgtgtac tgaggatcaa acctaggggc
 361 tcaagcagtc 900
 E--> 363 atcacaattc tctgtcactg atccagctcc atttctattt tcttttgtcc
 364 cgcgcgatct 960
 E--> 366 ctgcccagca agaaaacacg ctagggacat acgaatcctt gctgcagcca
 367 aaacttttat 1020
 E--> 369 tgaatcttaa ggagaagccc ggcacccgga ctggcgcggt ttatatacac
 370 cctagcacag 1080
 372 tgcattccaca 1090
 W--> 374 M:\clients\W\WPT\0114pusa\sequence list with pg #s.wpd
 E--> 375 sandy m. 7-21-00
 E--> 376 shelly 07/24/00
 E--> 378 -14-

same

delete at end of file

VERIFICATION SUMMARY
 PATENT APPLICATION: US/09/101,423

DATE: 08/09/2000
 TIME: 14:53:46

Input Set : A:\ES.txt
 Output Set: N:\CRF3\08092000\I101423.raw

L:5 M:283 W: Missing Blank Line separator, <120> field identifier
 L:6 M:283 W: Missing Blank Line separator, <130> field identifier
 L:7 M:283 W: Missing Blank Line separator, <140> field identifier
 L:11 M:283 W: Missing Blank Line separator, <160> field identifier
 L:19 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:50 SEQ:1
 L:19 M:112 C: (48) String data converted to lower case,
 M:112 Repeated in SeqNo=1
 M:254 Repeated in SeqNo=1
 L:78 M:282 W: Numeric Field Identifier Missing, <213> is required.
 L:79 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:50 SEQ:2
 M:112 Repeated in SeqNo=2
 M:254 Repeated in SeqNo=2
 L:140 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:50 SEQ:3
 M:112 Repeated in SeqNo=3
 M:254 Repeated in SeqNo=3
 L:198 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:50 SEQ:4
 M:112 Repeated in SeqNo=4
 M:254 Repeated in SeqNo=4
 L:263 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:50 SEQ:5
 M:112 Repeated in SeqNo=5
 M:254 Repeated in SeqNo=5
 L:317 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:50 SEQ:6
 M:112 Repeated in SeqNo=6
 M:254 Repeated in SeqNo=6
 L:374 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:5
 L:375 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:6
 L:375 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:6
 L:375 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:6
 L:375 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:6
 L:375 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:6
 L:375 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
 L:376 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:9
 L:378 M:252 E: No. of Seq. differs, <211>LENGTH:Input:1090 Found:1107 SEQ:6

RE ED
 AUG 18 2000
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